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RAW SEQUENCE LISTING

DATE: 03/13/2002

PATENT APPLICATION: US/09/910,706A

TIME: 11:16:34

Input Set : A:\JHU1520-2.TXT

Output Set: N:\CRF3\03132002\I910706A.raw

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4 <110> APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
5     WORLEY, Paul F.
6     BRAKEMAN, Paul R.
8 <120> TITLE OF INVENTION: SYNAPTIC ACTIVATION PROTEIN COMPOSITIONS AND METHOD
10 <130> FILE REFERENCE: JHU1520-2
12 <140> CURRENT APPLICATION NUMBER: US 09/910,706A
13 <141> CURRENT FILING DATE: 2001-07-20
15 <150> PRIOR APPLICATION NUMBER: US 09/042,428
16 <151> PRIOR FILING DATE: 1998-03-13
18 <150> PRIOR APPLICATION NUMBER: US 60/036,553
19 <151> PRIOR FILING DATE: 1997-03-14
21 <160> NUMBER OF SEQ ID NOS: 15
23 <170> SOFTWARE: PatentIn version 3.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 558
27 <212> TYPE: DNA
28 <213> ORGANISM: Rattus norvegicus
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31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)...(558)
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35 atg ggg gaa caa cct atc ttc agc act cga gct cat gtc ttc cag atc      48
36 Met Gly Glu Gln Pro Ile Phe Ser Thr Arg Ala His Val Phe Gln Ile
37 1      5      10      15
39 gac cca aac aca aag aag aac tgg gta ccc acc agc aag cat gca gtt      96
40 Asp Pro Asn Thr Lys Lys Asn Trp Val Pro Thr Ser Lys His Ala Val
41      20      25      30
43 act gtg tct tat ttc tat gac agc aca agg aat gtg tat agg ata atc      144
44 Thr Val Ser Tyr Phe Tyr Asp Ser Thr Arg Asn Val Tyr Arg Ile Ile
45      35      40      45
47 agt cta gac ggc tca aag gca ata ata aat agc acc atc act cca aac      192
48 Ser Leu Asp Gly Ser Lys Ala Ile Ile Asn Ser Thr Ile Thr Pro Asn
49      50      55      60
51 atg aca ttt act aaa aca tct caa aag ttt ggc caa tgg gct gat agc      240
52 Met Thr Phe Thr Lys Thr Ser Gln Lys Phe Gly Gln Trp Ala Asp Ser
53 65      70      75      80
55 cgg gca aac act gtt tat gga ctg gga ttc tcc tct gag cat cat ctc      288
56 Arg Ala Asn Thr Val Tyr Gly Leu Gly Phe Ser Ser Glu His His Leu
57      85      90      95
59 tca aaa ttt gca gaa aag ttt cag gaa ttt aaa gaa gct gct cgg ctg      336
60 Ser Lys Phe Ala Glu Lys Phe Gln Glu Phe Lys Glu Ala Ala Arg Leu
61      100      105      110
63 gca aag gag aag tcg cag gag aag atg gaa ctg acc agt acc cct tca      384

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64 Ala Lys Glu Lys Ser Gln Glu Lys Met Glu Leu Thr Ser Thr Pro Ser
65      115      120      125
67 cag gaa tca gca gga gga gat ctt cag tct cct tta aca cca gaa agt      432
68 Gln Glu Ser Ala Gly Gly Asp Leu Gln Ser Pro Leu Thr Pro Glu Ser
69      130      135      140
71 atc aat ggg aca gat gat gag aga aca ccc gat gtg aca cag aac tca      480
72 Ile Asn Gly Thr Asp Asp Glu Arg Thr Pro Asp Val Thr Gln Asn Ser
73 145      150      155      160
75 gag cca agg gct gag cca gct cag aat gca ttg cca ttt tca cat agg      528
76 Glu Pro Arg Ala Glu Pro Ala Gln Asn Ala Leu Pro Phe Ser His Arg
77      165      170      175
79 tac aca ttc aat tca gca atc atg att aaa      558
80 Tyr Thr Phe Asn Ser Ala Ile Met Ile Lys
81      180      185
84 <210> SEQ ID NO: 2
85 <211> LENGTH: 186
86 <212> TYPE: PRT
87 <213> ORGANISM: Rattus norvegicus
89 <400> SEQUENCE: 2
91 Met Gly Glu Gln Pro Ile Phe Ser Thr Arg Ala His Val Phe Gln Ile
92 1      5      10      15
93 Asp Pro Asn Thr Lys Lys Asn Trp Val Pro Thr Ser Lys His Ala Val
94      20      25      30
95 Thr Val Ser Tyr Phe Tyr Asp Ser Thr Arg Asn Val Tyr Arg Ile Ile
96      35      40      45
97 Ser Leu Asp Gly Ser Lys Ala Ile Ile Asn Ser Thr Ile Thr Pro Asn
98      50      55      60
99 Met Thr Phe Thr Lys Thr Ser Gln Lys Phe Gly Gln Trp Ala Asp Ser
100 65      70      75      80
101 Arg Ala Asn Thr Val Tyr Gly Leu Gly Phe Ser Ser Glu His His Leu
102      85      90      95
103 Ser Lys Phe Ala Glu Lys Phe Gln Glu Phe Lys Glu Ala Ala Arg Leu
104      100      105      110
105 Ala Lys Glu Lys Ser Gln Glu Lys Met Glu Leu Thr Ser Thr Pro Ser
106      115      120      125
107 Gln Glu Ser Ala Gly Gly Asp Leu Gln Ser Pro Leu Thr Pro Glu Ser
108      130      135      140
109 Ile Asn Gly Thr Asp Asp Glu Arg Thr Pro Asp Val Thr Gln Asn Ser
110 145      150      155      160
111 Glu Pro Arg Ala Glu Pro Ala Gln Asn Ala Leu Pro Phe Ser His Arg
112      165      170      175
113 Tyr Thr Phe Asn Ser Ala Ile Met Ile Lys
114      180      185
116 <210> SEQ ID NO: 3
117 <211> LENGTH: 50
118 <212> TYPE: PRT
119 <213> ORGANISM: Homo sapiens
121 <400> SEQUENCE: 3
123 Met Gly Glu Gln Pro Ile Phe Thr Thr Arg Ala His Val Phe Gln Ile

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124 1          5          10          15
125 Asp Pro Asn Thr Lys Lys Asn Trp Met Pro Ala Ser Lys His Gly His
126          20          25          30
127 Arg Phe Tyr Phe Tyr Asp Val Thr Arg Asn Ser Tyr Arg Ile Ile Ser
128          35          40          45
129 Val Asp
130          50
132 <210> SEQ ID NO: 4
133 <211> LENGTH: 153
134 <212> TYPE: PRT
135 <213> ORGANISM: Mus musculus
137 <400> SEQUENCE: 4
139 Tyr Phe Tyr Asp Val Thr Arg Asn Ser Tyr Arg Ile Ile Ser Val Asp
140 1          5          10          15
141 Gly Ala Lys Val Ile Ile Asn Ser Thr Ile Thr Pro Asn Met Thr Phe
142          20          25          30
143 Thr Lys Thr Ser Gln Lys Phe Gly Gln Trp Ala Asp Ser Arg Ala Asn
144          35          40          45
145 Thr Val Phe Gly Leu Gly Phe Ser Ser Glu Leu Gln Leu Thr Lys Phe
146          50          55          60
147 Ala Glu Lys Phe Gln Glu Val Arg Glu Ala Ala Arg Leu Ala Arg Asp
148 65          70          75          80
149 Lys Ser Gln Glu Lys Thr Glu Thr Ser Ser Asn His Ser Gln Glu Ser
150          85          90          95
151 Gly Cys Glu Thr Pro Ser Ser Thr Gln Ala Ser Ser Val Asn Gly Thr
152          100          105          110
153 Asp Asp Glu Lys Ala Ser His Ala Ser Pro Ala Asp Thr His Leu Lys
154          115          120          125
155 Ser Glu Asn Asp Lys Leu Lys Ile Ala Leu Thr Gln Ser Ala Ala Asn
156          130          135          140
157 Val Lys Lys Trp Glu Met Glu Leu Gln
158 145          150
160 <210> SEQ ID NO: 5
161 <211> LENGTH: 10
162 <212> TYPE: PRT
163 <213> ORGANISM: Artificial sequence
165 <220> FEATURE:
166 <223> OTHER INFORMATION: C-terminal of metabotropic glutamate receptor,
167 mGluR1-alpha.
169 <400> SEQUENCE: 5
171 Arg Asp Tyr Lys Gln Ser Ser Ser Thr Leu
172 1          5          10
174 <210> SEQ ID NO: 6
175 <211> LENGTH: 10
176 <212> TYPE: PRT
177 <213> ORGANISM: Artificial sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION: C-terminal of metabotropic glutamate receptor,
181 mGluR2.

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183 <400> SEQUENCE: 6
184 Glu Val Val Asp Ser Thr Thr Ser Ser Leu
185 1 5 10
187 <210> SEQ ID NO: 7
188 <211> LENGTH: 10
189 <212> TYPE: PRT
190 <213> ORGANISM: Artificial sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: C-terminal of metabotropic glutamate receptor,
194 mGluR3.
196 <400> SEQUENCE: 7
198 Glu Val Leu Asp Ser Thr Thr Ser Ser Leu
199 1 5 10
201 <210> SEQ ID NO: 8
202 <211> LENGTH: 10
203 <212> TYPE: PRT
204 <213> ORGANISM: Artificial sequence
206 <220> FEATURE:
207 <223> OTHER INFORMATION: C-terminal of metabotropic glutamate receptor,
208 mGluR4.
210 <400> SEQUENCE: 8
212 Thr Tyr Val Thr Tyr Thr Asn His Ala Ile
213 1 5 10
215 <210> SEQ ID NO: 9
216 <211> LENGTH: 10
217 <212> TYPE: PRT
218 <213> ORGANISM: Artificial sequence
220 <220> FEATURE:
221 <223> OTHER INFORMATION: C-terminal of metabotropic glutamate receptor,
222 mGluR5.
224 <400> SEQUENCE: 9
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227 1 5 10
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230 <211> LENGTH: 4
231 <212> TYPE: PRT
232 <213> ORGANISM: Artificial sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: peptide binding sequence
237 <400> SEQUENCE: 10
238 Ser Ser Thr Leu
239 1
241 <210> SEQ ID NO: 11
242 <211> LENGTH: 4
243 <212> TYPE: PRT
244 <213> ORGANISM: Artificial sequence
246 <220> FEATURE:
247 <223> OTHER INFORMATION: peptide binding sequence
249 <400> SEQUENCE: 11

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251 Ser Ser Ser Leu
252 1
254 <210> SEQ ID NO: 12
255 <211> LENGTH: 4
256 <212> TYPE: PRT
257 <213> ORGANISM: Rattus norvegicus
259 <220> FEATURE:
260 <221> NAME/KEY: VARIANT
261 <222> LOCATION: (0)...(0)
262 <223> OTHER INFORMATION: position 31-34 of SEQ ID NO:2
264 <400> SEQUENCE: 12
266 Ala Val Thr Val
267 1
269 <210> SEQ ID NO: 13
270 <211> LENGTH: 4
271 <212> TYPE: PRT
272 <213> ORGANISM: Homo sapiens / Mouse
274 <220> FEATURE:
275 <221> NAME/KEY: VARIANT
276 <222> LOCATION: (0)...(0)
277 <223> OTHER INFORMATION: positions 31-34 of SEQ ID NO:3
279 <400> SEQUENCE: 13
281 Gly His Arg Phe
282 1
284 <210> SEQ ID NO: 14
285 <211> LENGTH: 4
286 <212> TYPE: PRT
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: PDZ-like domain
292 <400> SEQUENCE: 14
294 Gly Leu Gly Phe
295 1
297 <210> SEQ ID NO: 15
298 <211> LENGTH: 4
299 <212> TYPE: PRT
300 <213> ORGANISM: Artificial Sequence
302 <220> FEATURE:
303 <223> OTHER INFORMATION: C-terminal motif
305 <400> SEQUENCE: 15
307 Thr Ser Ser Leu
308 1

VERIFICATION SUMMARY

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